Serial Interval and Transmission Dynamics during SARS-CoV-2 Delta Variant Predominance, South Korea

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We estimated mean serial interval and superspreading potential for the Delta variant of severe acute respiratory syndrome coronavirus 2 in South Korea. Intervals were similar for the first (3.7 days) and second (3.5 days) study periods. Risk for superspreading events was also similar; 23% and 25% of cases, respectively, seeded 80% of transmissions.

As of August 2021, South Korea is in the middle of a fourth community epidemic of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission, which is now predominated by the B.1.617.2 lineage (Delta variant) (*1,2*). The epidemic size largely depends on such epidemiologic characteristics as serial interval distribution and transmissibility (*3,4*). For the Delta variant of SARS-CoV-2, however, empirical evidence produced using country-level data are limited. We estimated serial interval distribution, reproductive numbers, and superspreading potential of SARS-CoV-2 during the Delta variant predominance in South Korea.

The Study

We obtained line-list data on coronavirus disease (COVID-19) cases reported by South Korea local public health authorities during July 11, 2021–September 1, 2021. Because the detection rate of the Delta variant accounted for >50% of local cases after July 25, 2021, and to avoid right-censoring bias, we divided the study duration into 2 periods (period 1, July 11, 2021–July 24, 2021; period 2, July 25, 2021–August 15, 2021). Overall, 82,671 local cases were obtained during the

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whole study period; 19,635 cases were identified in period 1, and 34,569 cases were identified in period 2. The data included information on contact tracing with other reported cases of COVID-19 (i.e., the case number of infector or infectee) and dates of symptom onset. The serial interval represents the time between symptom onset for both the infector and the infectee in a transmission chain (*3*). On the basis of line-list information, we reconstructed the transmission pairs by identifying the infector and infectee. We identified 3,728 transmission pairs (1,344 pairs in period 1 and 2,384 pairs in period 2) having the date of symptom onset for both infector and infectee. The overall mean of the serial interval estimate was 3.6 days (95% credible interval [CrI] 3.5–3.6 days) and the SD of the serial interval estimate was 4.9 days (95% CrI 4.9–5.0 days). The mean serial interval estimate were 3.7 (95% CrI 3.5–3.8) days with an SD of 4.8 (95% CrI 4.8–4.9) days during period 1, and 3.5 (95% CrI 3.4–3.6) days with an SD of 5.0 (95% CrI 4.9–5.0) days during period 2 (Figure 1, panel A). We used Welch's 2-sample t-test to compare the mean serial intervals for period 1 and period 2 and found no significant difference (p value = 0.40).

To identify the potential changes in SARS-CoV-2 transmissibility, we estimated the time-varying effective reproductive number (R_t), which defines the mean number of secondary infectious cases generated from a typical primary infectious case at time *t*. The epidemic becomes under control if R_t falls below 1 sustainably. We estimated R_t by using the EpiEstim package in R (*5*). In South Korea, nonpharmaceutical interventions including a nationwide mask mandate have been implemented since 2020. Because a large number of COVID-19 cases were identified by mid-July 2021, a 4-person limit for gatherings was implemented beginning July 19, 2021, nationwide (*6*) (Figure 1, panels B and C). However, we identified that

Figure 1. Estimated serial interval distribution, incidence of coronavirus disease, and transmissibility during predominance of the Delta variant of severe acute respiratory syndrome coronavirus 2 in South Korea. A) Estimated serial interval distribution for 3,728 infector-infectee pairs. Solid blue line indicates fitted normal distribution; vertical bars indicate the distribution of empirical serial intervals. B) Reported number of confirmed coronavirus disease cases by date of symptom onset. Red vertical dashed line indicates the date of implementation of an enhanced social distancing, including limiting gathering sizes to 4 persons nationwide on July 19, 2021. C) Estimated daily R_t of severe acute respiratory syndrome coronavirus 2 (blue line) with 95% credible intervals (gray shade). Gray horizontal dashed line indicates the critical threshold of $R_t = 1$. Red vertical dashed line indicates the date of implementation of an enhanced social distancing. R_t, effective reproductive number.
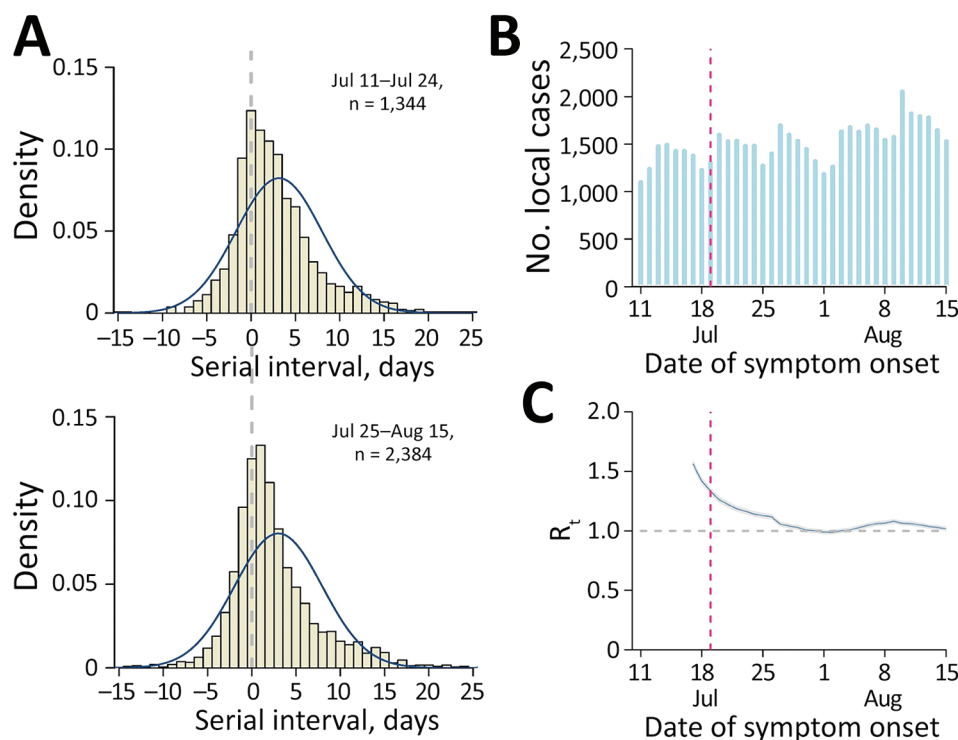
the estimated R_t was sustained at >1 during the study period (Figure 1, panel C).

To analyze superspreading potential, we identified 5,778 transmission pairs that included the COVID-19 cases for which no date of symptom onset was provided for either infector or infectee (2,169 pairs for period 1 and 3,609 pairs for period 2). We calculated the number of secondary cases for each person from the transmission pairs and fitted the data into a negative binomial distribution (7) (Appendix, https://wwwnc.cdc.gov/EID/article/28/2/21-1774-App1.pdf). The 2 parameters of the distribution represent the reproduction number (R_0) and overdispersion parameter (k). The estimated k for period 1 was 0.64 (95% CrI 0.57–0.72) and for period 2 was 0.85 (95% CrI 0.75–0.98), which corresponded to an expected percentage of cases responsible for 80% of secondary cases of 23% (95% CrI 22%–24%) for period 1 and 25% (95% CrI 24%–26%) for period 2 (Figure 2).

Conclusions

We estimated the serial interval distributions of SARS-CoV-2 for early and later periods of the Delta variant predominance in South Korea and identified that mean serial intervals were similar across 2 different periods. This similarity is consistent with a recent study suggesting no substantial differences in the serial intervals between patients infected with the Delta variant and wild-type virus (8). In contrast, however, our findings suggested that the mean serial interval was 1 day longer than the estimates reported in a study describing the faster spread of the Delta
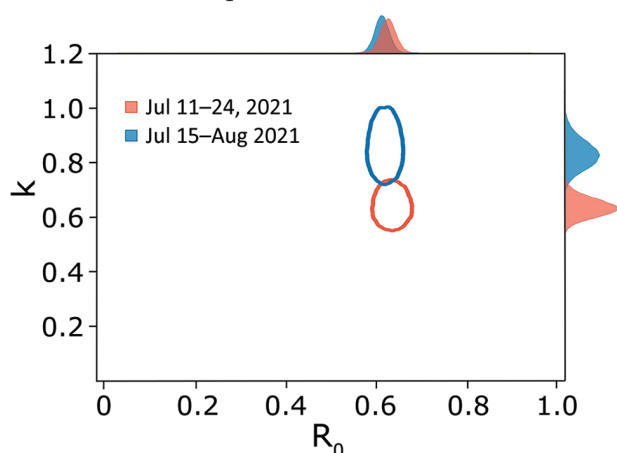
Figure 2. Risk for superspreading events for coronavirus disease during the Delta variant of severe acute respiratory syndrome coronavirus 2 predominance in South Korea. Joint estimates of k and R_0 of coronavirus disease were calculated by using 5,778 pairs (2,169 for period 1 and 3,609 for period 2). The red and blue ovals indicate the bivariate 95% credible region of the estimated k and R_0 for period 1 and period 2. The posterior marginal distributions were plotted in red and blue shaded regions. Period 1, July 11, 2021–July 24, 2021; period 2, July 25, 2021–August 15, 2021. k, overdispersion parameter; R_0, basic reproduction number.

variant in China (mean serial interval of 2.3 days) compared with the wild type (*9*). Changes to public health measures, such as active contact tracing and rapid isolation of COVID-19 patients, would have shortened the serial interval and reduced transmissibility and superspreading potential (*3,4*). Since June 10, 2020, however, the South Korean public health authority has consistently implemented strategies for active case finding and immediately isolating laboratory-confirmed COVID-19 patients and exposed persons by using digital QR codes (*10*). Therefore, the effect of enhanced case isolation against the serial interval of SARS-CoV-2 is likely limited in our study. Furthermore, restricting large gatherings had likely reduced the superspreading potential. However, because the R_t was >1 during most of the study period, the nonpharmaceutical interventions implemented were likely insufficient to control the transmission of SARS-CoV-2 in South Korea.

Our study's first limitation is that we did not consider the effect of COVID-19 vaccinations in our analysis. About 14% of transmission pairs used in this study were linked with older adults ($\geq$60 years of age), who might have received COVID-19 vaccinations. However, the vaccination program was not implemented in members of the public <55 years of age in early August 2021. Second, we did not consider changes in nonpharmaceutical interventions on the local level and possible increased travel during the study period, because it included summer holidays. Enhanced social distancing, however, including limiting gatherings to 4 persons, was in place nationwide during the study period. Third, we retrieved online case reports, which could contain some inaccuracies. However, the daily number of laboratory-confirmed local cases was similar between the collected line list and official daily reports (Appendix). Last, because individual genotype information was not included in the line-list data, the proportion of the Delta variant was evaluated from alternative data retrieved from the Korea Disease Control and Prevention Agency.

A previous study from South Korea, which examined the early transmissibility of SARS-CoV-2 in February–March 2020, estimated the mean R_0 as 1.5 for the wild type (*11*), and the early epidemic of COVID-19 was successfully controlled with nonlockdown social distancing (*12*). Our findings suggest that the introduction of the Delta variant is likely to have increased the difficulty of controlling SARS-CoV-2 transmission in South Korea. The large number of COVID-19 cases in South Korea during the study period could be explained by the increased secondary attack rate generated by cases of the Delta variant (*13,14*), which is in line with a previous study (*8*). Encouraging COVID-19 vaccination and further strengthening nonpharmaceutical interventions are warranted to mitigate spread of the Delta variant.

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About the Author

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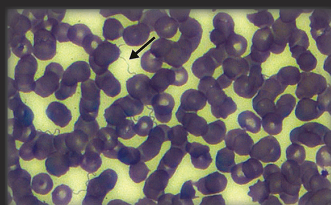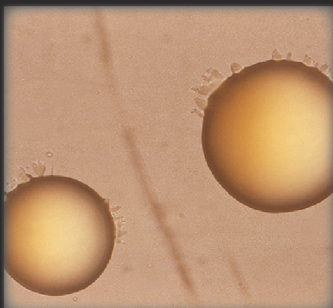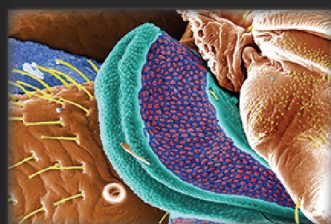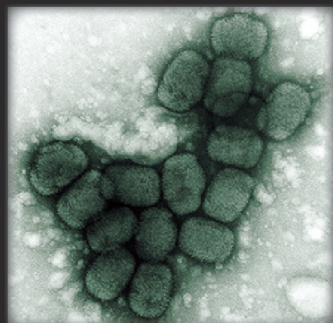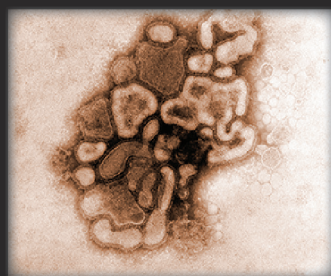
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Appendix

Data

We acquired data on coronavirus disease (COVID-19) cases, confirmed by real-time reverse transcription PCR (rRT-PCR) and reported by South Korea local public health authorities. The COVID-19 cases included occurred during July 11, 2021–September 1, 2021, when the Delta variant accounted for >40% of local cases reported from the Korea Disease Control and Prevention Agency (*1,2*). The data included contact tracing with other reported cases of COVID-19 and demographic characteristics of the patients, including age, sex, and date of symptom onset (https://github.com/gentryu/COVID-19delta).

Estimating Overdispersion Parameter (*K*)

Statistical methods used in this study followed our previous COVID-19 study for superspreading events (SSE) (*3*). The probability function of negative binomial distribution that an index case (i) generate the number of secondary case (y_i) is given by

$$Pr(Y = y_i) = \frac{\Gamma(k + y_i)}{y_i!\,\Gamma(k)}\left(\frac{k}{k + R}\right)^k \left(\frac{R}{k + R}\right)^{y_i},$$

where k and R are the estimated dispersion parameter and reproduction number, respectively, of index case i.

To understand the individual variation of infectiousness of COVID-19 during study period, observed offspring distributions were fitted to the negative binomial distribution. Given the estimated reproduction number and dispersion parameter, the proportion of infected persons responsible for 80% of secondary cases, $P_{80\%}$, was calculated by using equations from the previous studies (3–6). The proportion $P_{80\%}$ is given by

$$1 - P_{80\%} = \int_0^X NB\left(\lfloor x \rfloor; k, \frac{k}{R+k}\right) dx,$$

where X satisfies

$$1 - 0.80 = \frac{1}{R} \int_0^X \lfloor x \rfloor\, NB\left(\lfloor x \rfloor; k, \frac{k}{R+k}\right) dx.$$

Furthermore, with the threshold for SSE as 6 secondary cases defined in the previous study (4), the proportion of SSE was estimated for each period with the equations below.

$$\int_6^\infty NB\left(\lfloor x \rfloor; k, \frac{k}{R+k}\right) dx = 1 - \int_0^5 NB\left(\lfloor x \rfloor; k, \frac{k}{R+k}\right) dx.$$

Finally, using the branching process, the expected probability that 1 index case of SARS-CoV-2 infection results in a cluster of size s were estimated with the equations from previous studies (3,5,6) given by

$$r_s = \frac{\Gamma(ks+s-1)}{\Gamma(ks)\Gamma(s+1)}\left(\frac{R}{k}\right)^{s-1}\left(\frac{k}{k+R}\right)^{ks+s-1},$$

where the probability of cluster of size s or greater could be estimated as follows:

$$p_s = 1 - \sum_{l=1}^{s-1} r_l.$$

With the condition that N seed cases were introduced into the totally susceptible populations, the estimated probability that ≥ 1 cluster of size s or greater occurs is

$$P_{N,s} = 1 - (1 - p_s)^N.$$

Note that $P_{N,s}$ is equal to p_s when exactly 1 index case was introduced ($N = 1$).

We used a Bayesian Markov Chain Monte Carlo simulation using *rstan* package. Four chains of 40,000 iterations were obtained with 5,000 burn-in. The prior distributions of dispersion parameter and reproduction number were uniform with lower and upper bounds set at 0 and 100. Convergence was checked visually by using a trace plot and the Gelman–Rubin–Brooks diagnostic (*7*). The posterior distribution of the estimates was demonstrated with the median and 95% credible intervals (CrI).

Supplementary Analysis for the Risk for Superspreading Events

We estimated the expected proportion of cases responsible for 80% of the total secondary cases to identify the risk of SSE. Furthermore, we estimated the probability of SSEs using estimated R_0 and k and the probability that 1 index case results in a cluster of ≥ 10 cases.

Based on the source of infection, we estimate the offspring distribution using infectee-infector pairs. We fitted observed distribution of the secondary case into a negative binomial offspring distribution (Appendix Figure 1). The expected proportion of cases responsible for 80% of secondary cases was 22.99% (95% CrI 21.97%–24.03%) for period 1 and 24.93% (95% CrI 23.90%–25.97%) for period 2. The probability of SSE and the probability that 1 index case results in a cluster of ≥ 10 cases were 0.33% (95% CrI 0.25%–0.45%) and 4.71% (95% CrI 3.92%–5.60%) for period 1, and 0.17% (95% CrI 0.12%–0.24%) and 4.254% (95% CrI 3.51%–5.11%) for period 2.

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Appendix Table 1. Age-specific distribution of SARS-CoV-2 infector-infectee pairs having symptom onset for both infector and infectee, South Korea*

Age group of infector, y	Age group of infectee, y								
	0–9	10–19	20–29	30–39	40–49	50–59	≥60	NA	Total
0–9	16	16	26	32	20	34	8	1	153
10–19	18	51	82	57	78	45	42	0	373
20–29	48	76	160	119	130	126	52	3	714
30–39	41	57	134	133	103	87	34	2	591
40–49	41	67	112	84	103	115	49	1	572
50–59	34	47	125	96	103	113	60	2	580
≥60	21	31	61	43	43	44	38	1	282
NA	0	3	2	0	1	5	2	450	463
Total	219	348	702	564	581	569	285	460	3,728

*NA, not available; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

Appendix Table 2. Age-specific distribution of SARS-CoV-2 infector-infectee pairs for whom no date of symptom onset was reported for either infector or infectee, South Korea*

Age group of infector, y	Age group of infectee, y								
	0–9	10–19	20–29	30–39	40–49	50–59	≥60	NA	Total
0–9	36	31	46	58	41	66	19	4	301
10–19	37	62	107	80	109	79	60	0	534
20–29	86	107	234	170	196	179	82	4	1,058
30–39	73	87	195	188	144	136	73	3	899
40–49	64	103	159	127	161	187	75	3	879
50–59	71	84	188	151	139	192	104	3	932
≥60	29	53	117	71	67	79	68	2	486
NA	0	4	7	0	1	6	4	667	689
Total	396	531	1,053	845	858	924	485	686	5,778

*NA, not available; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.
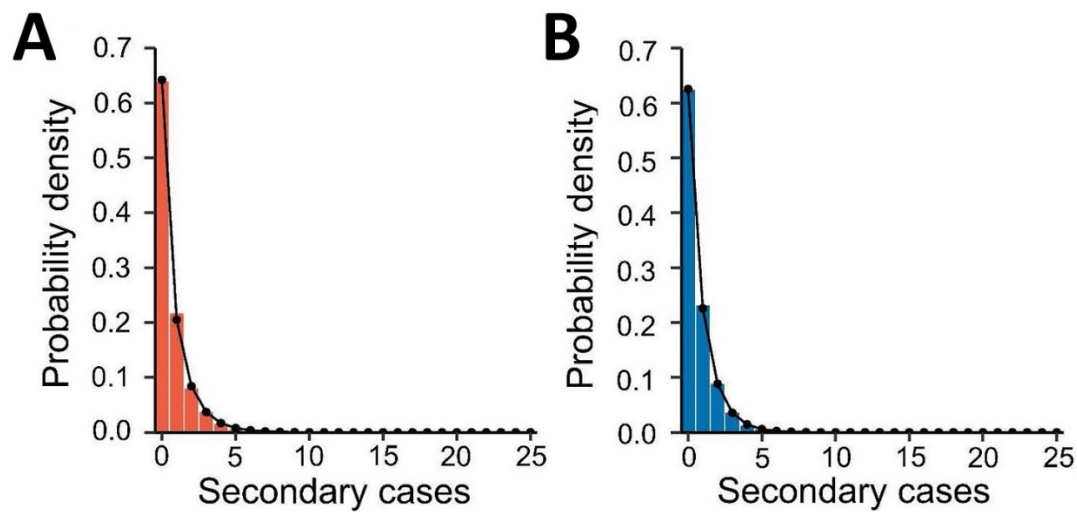
Appendix Figure 1. Distributions of the number of secondary cases of coronavirus disease in A) period 1 (July 11, 2021–July 24, 2021) and B) period 2 (July 25, 2021–August 15, 2021) and corresponding fitted negative binomial distributions, South Korea.
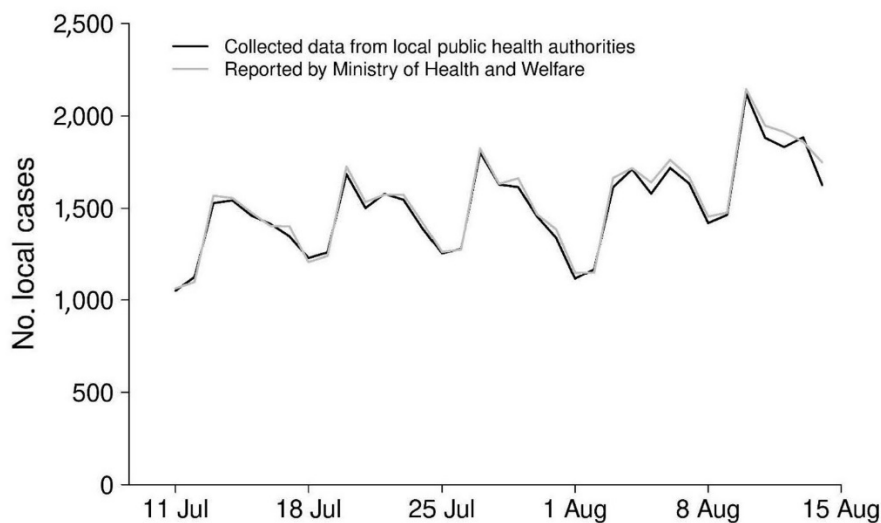
Appendix Figure 2. Daily number of coronavirus disease cases from the collected data and reported number by the Korean Ministry of Health and Welfare, South Korea. The black line indicates data collected from the local public health authority. The gray line indicates the daily number of coronavirus disease cases reported by the South Korean central government.